

OIIPE

RAW SEQUENCE LISTING

DATE: 05/30/2001

PATENT APPLICATION: US/09/820,843A

TIME: 11:46:43

Input Set : A:\PTO.txt

Output Set: C:\CRF3\05302001\I820843A.raw

P.5

3 <110> APPLICANT: Council of Scientific and Industrial Research

5 <120> TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE

PROTEINS

6 USEFUL AS ANTI-INFECTIVES

8 <130> FILE REFERENCE: Q63915

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/820,843A

C--> 10 <141> CURRENT FILING DATE: 2001-03-30

10 <160> NUMBER OF SEQ ID NOS: 118

12 <170> SOFTWARE: PatentIn version 3.0

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 51

16 <212> TYPE: PRT

17 <213> ORGANISM: C. jejuni

19 <220> FEATURE:

20 <221> NAME/KEY: misc_feature

21 <223> OTHER INFORMATION: highly acidic protein

24 <220> FEATURE:

25 <221> NAME/KEY: misc_feature

26 <223> OTHER INFORMATION: gi|6967728

29 <400> SEQUENCE: 1

31 Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn

32 1 5 10 15

34 Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp

35 20 25 30

37 Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Asp Phe Tyr

38 35 40 45

40 Glu Met Asp

41 50

43 <210> SEQ ID NO: 2

44 <211> LENGTH: 32

45 <212> TYPE: PRT

46 <213> ORGANISM: C. jejuni

48 <220> FEATURE:

49 <221> NAME/KEY: misc_feature

50 <223> OTHER INFORMATION: small hydrophobic protein

53 <220> FEATURE:

54 <221> NAME/KEY: misc_feature

55 <223> OTHER INFORMATION: gi|6969129

58 <400> SEQUENCE: 2

60 Met Thr Met Leu Asp Ile Phe Glu Ile Ile Phe Ile Thr Thr Val Val

61 1 5 10 15

63 Ile Ile Gly Phe Gly Gly Ile Val Phe Val Val Thr Lys Glu Lys Lys

64 20 25 30

66 <210> SEQ ID NO: 3

67 <211> LENGTH: 57

68 <212> TYPE: PRT

69 <213> ORGANISM: C. jejuni

71 <220> FEATURE:

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72 <221> NAME/KEY: misc_feature
73 <223> OTHER INFORMATION: putative coiled coil protein
76 <220> FEATURE:
77 <221> NAME/KEY: misc_feature
78 <223> OTHER INFORMATION: gi|6968493
81 <400> SEQUENCE: 3
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84 1          5          10          15
86 Leu Asn Asn Gln Glu Leu Ala Leu Asp Glu Ser Val Lys Ile Tyr Lys
87          20          25          30
89 Glu Gly Leu Glu Ser Ile Lys Lys Ala Arg Leu Glu Leu Glu Lys Ala
90          35          40          45
92 Lys Leu Glu Val Glu Gln Ile Asp Glu
93          50          55
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 542
97 <212> TYPE: PRT
98 <213> ORGANISM: C. jejuni
100 <220> FEATURE:
101 <221> NAME/KEY: misc_feature
102 <223> OTHER INFORMATION: highly acidic protein
105 <220> FEATURE:
106 <221> NAME/KEY: misc_feature
107 <223> OTHER INFORMATION: gi|6968611
110 <400> SEQUENCE: 4
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113 1          5          10          15
115 Ser Leu Ser Ala Lys Lys Met Ser Tyr Asp Phe Glu Glu Leu Asn Ala
116          20          25          30
118 Tyr Ser Glu Asn Leu Gly Asn Tyr Asp Val Ile Val Val Asp Ser Asp
119          35          40          45
121 Thr Pro Ala Pro Leu Lys Ile Leu Lys Glu Lys Cys Asp Arg Leu Ile
122          50          55          60
124 Phe Leu Ala Pro Arg Asn Gln Asn Val Glu Asp Ile Asp Ala Gln Ile
125 65          70          75          80
127 Leu Gln Lys Pro Phe Leu Pro Thr Asp Phe Leu Asn Leu Leu Asn Asn
128          85          90          95
130 Lys Asp Ala Asn Lys His Thr Ser Ile Asp Leu Pro Met Leu Ser Asn
131          100          105          110
133 Asp Glu Asn Pro Tyr Ala Asp Ile Ser Leu Asp Leu Asp Asn Leu Asn
134          115          120          125
136 Leu Asp Asp Leu Pro Asp Glu Asn Ser Leu Asp Ile Asn Ser Glu Gly
137          130          135          140
139 Met Glu Asp Leu Ser Phe Asp Asp Asp Ala Gln Asp Asp Asn Ala Asn
140 145          150          155          160
142 Lys Thr Leu Glu Thr Gln Asn Leu Glu His Glu Thr Ile Lys Glu Gln
143          165          170          175
145 Thr Gln Glu Asp Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly
146          180          185          190

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148 Glu Ser Glu Lys Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr
149      195      200      205
151 Glu Pro Ser Leu Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu
152      210      215      220
154 Ile Lys Glu Asp Asp Lys Asn Glu Glu Ile Glu Lys Gln Glu Leu Leu
155 225      230      235      240
157 Asp Asp Ser Lys Thr Asn Thr Leu Glu Met Gln Glu Glu Leu Ser Glu
158      245      250      255
160 Ser Gln Asp Asp Asn Ser Asn Lys Thr Leu Glu Thr Gln Asn Leu Glu
161      260      265      270
163 His Asp Asn Leu Glu Gln Glu Thr Ile Lys Glu Gln Thr Gln Glu Asp
164      275      280      285
166 Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly Glu Ser Glu Lys
167      290      295      300
169 Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr Glu Pro Ser Leu
170 305      310      315      320
172 Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu Asp Asn Lys Glu
173      325      330      335
175 Leu Gln Ala Asn Ile Ser Asp Phe Asp Asp Leu Pro Glu Val Glu Glu
176      340      345      350
178 Gln Glu Lys Glu Met Asp Phe Asp Asp Leu Pro Glu Asp Ala Glu Phe
179      355      360      365
181 Leu Gly Gln Ala Lys Tyr Asn Glu Glu Ser Glu Glu Asn Leu Glu Glu
182      370      375      380
184 Phe Ala Pro Val Val Glu Glu Asp Ile Gln Asp Glu Ile Asp Asp Phe
185 385      390      395      400
187 Ala Ser Asn Leu Ser Thr Gln Asp Gln Ile Lys Glu Glu Leu Ala Gln
188      405      410      415
190 Leu Asp Glu Leu Asp Tyr Gly Ile Asp Ser Asp Asn Ser Ser Lys Val
191      420      425      430
193 Leu Glu Asp Phe Lys Asp Glu Pro Ile Leu Asp Asp Lys Glu Leu Gly
194      435      440      445
196 Thr Asn Glu Glu Glu Val Val Val Pro Asn Leu Asn Ile Ser Asp Phe
197      450      455      460
199 Asp Thr Leu Lys Glu Ser Asp Ile Gln Glu Ala Leu Gly Glu Glu Ile
200 465      470      475      480
202 Leu Glu Lys Asn Glu Glu Pro Ile Val Ser Asp Val Thr Lys Asp Asp
203      485      490      495
205 Asn Ser Glu Glu Ile Val Asn Glu Leu Ser Gln Ser Ile Ala Gly Ala
206      500      505      510
208 Ile Thr Ser Ser Ile Lys Asp Asp Thr Leu Lys Ala Ala Leu Lys Gly
209      515      520      525
211 Met Asn Met Asn Ile Asn Ile Asn Ile Ser Phe Lys Glu Asp
212      530      535      540
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 172
216 <212> TYPE: PRT
217 <213> ORGANISM: C. pneumoniaeCWL029
219 <220> FEATURE:

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220 <221> NAME/KEY: misc_feature
221 <223> OTHER INFORMATION: histone like protein 2
224 <220> FEATURE:
225 <221> NAME/KEY: misc_feature
226 <223> OTHER INFORMATION: gi|4376663
229 <400> SEQUENCE: 5
231 Met Ile Gly Ala Gln Lys Lys Gln Ser Gly Lys Lys Thr Ala Ser Arg
232 1 5 10 15
234 Ala Val Arg Lys Pro Ala Lys Lys Val Ala Ala Lys Arg Thr Val Lys
235 20 25 30
237 Lys Ala Thr Val Arg Lys Thr Ala Val Lys Lys Pro Ala Val Arg Lys
238 35 40 45
240 Thr Ala Ala Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Thr
241 50 55 60
243 Val Arg Lys Thr Val Ala Lys Lys Pro Ala Val Lys Lys Val Ala Ala
244 65 70 75 80
246 Lys Arg Val Val Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg
247 85 90 95
249 Ala Val Arg Lys Thr Val Ala Lys Lys Pro Val Ala Arg Lys Thr Thr
250 100 105 110
252 Val Ala Lys Gly Ser Pro Lys Lys Ala Ala Ala Cys Ala Leu Ala Cys
253 115 120 125
255 His Lys Asn His Lys His Thr Ser Ser Cys Lys Arg Val Cys Ser Ser
256 130 135 140
258 Thr Ala Thr Arg Lys His Gly Ser Lys Ser Arg Val Arg Thr Ala His
259 145 150 155 160
261 Gly Trp Arg His Gln Leu Ile Lys Met Met Ser Arg
262 165 170
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 63
266 <212> TYPE: PRT
267 <213> ORGANISM: C. trachomatis
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <223> OTHER INFORMATION: hypothetical protein-possible frameshift with CT593
274 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
276 <223> OTHER INFORMATION: gi|3522902
279 <400> SEQUENCE: 6
281 Met Phe Thr Leu Phe Leu Cys Glu His Leu Leu Thr Asn Ile Leu Ala
282 1 5 10 15
284 Ser Ser Phe Leu Ala Lys Ser Gln Gly Phe Ile Thr Leu Val Asn Leu
285 20 25 30
287 Phe His Lys Ile Pro Gly Leu Lys Val Ile Glu Ile Thr Cys Leu Ala
288 35 40 45
290 Leu Pro Leu Gly Ile His Ser Ile Ile Gly Phe Ser Tyr Leu Leu
291 50 55 60
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 203

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295 <212> TYPE: PRT
 296 <213> ORGANISM: C. trachomatis
 298 <220> FEATURE:
 299 <221> NAME/KEY: misc_feature
 300 <223> OTHER INFORMATION: histone like protein 2
 303 <220> FEATURE:
 304 <221> NAME/KEY: misc_feature
 305 <223> OTHER INFORMATION: gi|3328438
 308 <400> SEQUENCE: 7
 310 Met Asn Met Leu Gly Val Gln Lys Lys Cys Ser Thr Arg Lys Thr Ala
 311 1 5 10 15
 313 Ala Arg Lys Thr Val Val Arg Lys Pro Ala Ala Lys Lys Thr Ala Ala
 314 20 25 30
 316 Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys Thr Val Ala Arg
 317 35 40 45
 319 Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys Pro Val Ala Lys
 320 50 55 60
 322 Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys
 323 65 70 75 80
 325 Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys
 326 85 90 95
 328 Pro Val Ala Lys Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Ala
 329 100 105 110
 331 Val Ala Lys Lys Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val
 332 115 120 125
 334 Ala Ala Arg Lys Pro Val Ala Lys Arg Val Ala Ser Thr Lys Lys Ser
 335 130 135 140
 337 Ser Ile Ala Val Lys Ala Gly Val Cys Met Lys Lys His Lys His Thr
 338 145 150 155 160
 340 Ala Ala Cys Gly Arg Val Ala Ala Ser Gly Val Lys Val Cys Ala Ser
 341 165 170 175
 343 Ala Ala Lys Arg Lys Thr Asn Pro Asn Arg Ser Arg Thr Ala His Ser
 344 180 185 190
 346 Trp Arg Gln Gln Leu Met Lys Leu Val Ala Arg
 347 195 200
 349 <210> SEQ ID NO: 8
 350 <211> LENGTH: 372
 351 <212> TYPE: PRT
 352 <213> ORGANISM: H. influenzae
 354 <220> FEATURE:
 355 <221> NAME/KEY: misc_feature
 356 <223> OTHER INFORMATION: outer membrane integrity protein (tolA)
 359 <220> FEATURE:
 360 <221> NAME/KEY: misc_feature
 361 <223> OTHER INFORMATION: gi|1573353
 364 <400> SEQUENCE: 8
 366 Met Gln Asn Asn Arg Gln Lys Lys Gly Ile Asn Ala Phe Ala Ile Ser
 367 1 5 10 15
 369 Ile Leu Leu His Phe Ile Leu Phe Gly Leu Leu Ile Leu Ser Ser Leu

Please Note:

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

file://C:\Crf3\Outhold\VsrI820843A.htm

5/30/01

VERIFICATION SUMMARY

DATE: 05/30/2001

PATENT APPLICATION: US/09/820,843A

TIME: 11:46:44

Input Set : A:\PTO.txt

Output Set: C:\CRF3\05302001\I820843A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2891 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32

L:2891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32

L:4698 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66

L:4698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66